

**EXHIBIT A:**

**MOUSE LKB1 COMPARED TO HUMAN LKB1**

## BLAST

## Basic Local Alignment Search Tool

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

## SEQ ID NO: 6 (44-343) Compared to Mouse LKB1

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

## Query ID

ic|41549  
ic|41549

## Description

SEQ ID NO: 6

## Molecule type

amino acid

## Query Length

433

## Subject ID

gi|7106425|ref|NP\_035622.1|

## Description

serine/threonine-protein kinase 11 [Mus musculus] >gi|81917862|sp|Q9WTK7.1|STK11\_MOUSE RecName: Full=Serine/threonine-protein kinase 11; AltName: Full=Serine/threonine-protein kinase LKB1 >gi|4838565|gb|AAD31044.1|AF145287.1 Peutz-Jeghers syndrome kinase LKB1 [Mus musculus] >gi|6649101|gb|AAF21370.1|AF151711.1 protein kinase LKB1 [Mus musculus] >gi|4530575|gb|AAD22100.1| serine/threonine-protein kinase LKB1 [Mus musculus] >gi|4589404|dbj|BAA76749.1| LKB1 [Mus musculus] >gi|5901683|gb|AAD55368.1| Peutz-Jeghers syndrome protein [Mus musculus] >gi|30851173|gb|AAH52379.1| Serine/threonine kinase 11 [Mus musculus] >gi|74186437|dbj|BAE42977.1| unnamed protein product [Mus musculus] >gi|74192527|dbj|BAE43050.1| unnamed protein product [Mus musculus] >gi|117616790|gb|ABK42413.1| Stk11 [synthetic construct] >gi|148699653|gb|EDL31600.1| serine/threonine kinase 11, isoform CRA\_a [Mus musculus]

## Molecule type

amino acid

## Subject Length

436

## Program

BLASTP 2.2.24+ [Citation](#)

## Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

## Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Multiple alignment](#)

[Search Parameters](#)

## Search parameter name Search parameter value

Program	blastp
Query range	44-343
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

## Params Ungapped Gapped

Lambda	0.320459	0.267
K	0.139595	0.041
H	0.429592	0.14

Results Statistics

## Results Statistics parameter name Results Statistics parameter value

Effective search space	110297
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## **Graphic Summary**

### **Distribution of Blast Hits on the Query Sequence**

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

[Dot Matrix View](#)**Plot of lcl|41549 vs gi|7106425|ref|NP\_035622.1| [?] [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Sequences producing significant alignments:	Score (Bits)	E Value
<a href="#">ref NP_035622.1 </a> serine/threonine-protein kinase 11 [Mus musc...	526	4e-154

**Alignments**

```
>ref|NP_035622.1| serine/threonine-protein kinase 11 [Mus musculus]
sp|Q9WTK7.1|STK11_MOUSE RefName: Full-Serine/threonine-protein kinase 11; AltName: Full-Serine/threonine-protein kinase LKB1
gb|AAD31044.1|AP145287.1 Peutz-Jeghers syndrome kinase LKB1 [Mus musculus]
9 more sequence titles
```

```
gb|AAF21370.1|AF151711.1 protein kinase LKB1 [Mus musculus]
gb|AAD22100.1| serine/threonine-protein kinase LKB1 [Mus musculus]
db|BAA76749.1| LKB1 [Mus musculus]
gb|AAD55368.1| Peutz-Jeghers syndrome protein [Mus musculus]
gb|AAH52379.1| Serine/threonine kinase 11 [Mus musculus]
db|BAH42977.1| unnamed protein product [Mus musculus]
db|BAE43050.1| unnamed protein product [Mus musculus]
gb|ABK42413.1| Stk11 [synthetic construct]
gb|EDL31600.1| serine/threonine kinase 11, isoform CRA_a [Mus musculus]
Length=436
```

Score = 526 bits (1354), Expect = 4e-154, Method: Compositional matrix adjust.  
Identities = 288/300 (96%), Positives = 292/300 (98%), Gaps = 0/300 (0%)

Query	44	KLIGKYLMDLLGEGSYGKVKVLDSETLCRRVKKILKKKKLRRIPNGEANVKKEIQLLR	103
Sbjct	44	KLIGKYLMDLLGEGSYGKVKVLDSETLCRRVKKILKKKKLRRIPNGEANVKKEIQLLR	103
Query	104	RLRHKNVIQIVDVLYNEEKQKMYMMEYCVCGMQEMLDSVPEKRFVQCQAHGYFCQLIDG	163
Sbjct	104	RLRHKNVIQIVDVLYNEEKQKMYMMEYCVCGMQEMLDSVPEKRFVQCQAHGYFCQLIDG	163
Query	164	LEYLHSGQIVHKDIKPGNLLTTGGTISKISDLGVAEALHPFAADDCRTSQGSPAFQPPPE	223
Sbjct	164	LEYLHSGQIVHKDIKPGNLLTTGGTISKISDLGVAEALHPFAADDCRTSQGSPAFQPPPE	223
Query	224	IANGLDTFSGFKVDIWSAGVTLYNITTGLYFFEGDNIYKLFENIGKGSYAI PGDCGPPLS	283
Sbjct	224	IANGLDTFSGFKVDIWSAGVTLYNITTGLYFFEGDNIYKLFENIG+G + IP DCGPPLS	283
Query	284	DLLKGMLEYEPAKRFSIRQIRQHSWFRKKHppacavpippspDTKDRWRSMTVVVPYLED	343
Sbjct	284	DLLKGMLEYEPAKRFSIRQIRQHSWFRKKHPLAEALVPIPPSPDTKDRWRSMTVVVPYLED	343